

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Gentz, Reiner  
Fleischmann, Robert D.
- (ii) TITLE OF INVENTION: 5-LIPOXYGENASE-ACTIVATING PROTEIN II
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: JAMES H. DAVIS  
HUMAN GENOME SCIENCES, INC.
  - (B) STREET: 9410 KEY WEST AVENUE
  - (C) CITY: ROCKVILLE
  - (D) STATE: MD
  - (E) COUNTRY: USA
  - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: DIVISIONAL OF US 08/264,003
  - (B) FILING DATE: HERewith
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: JONATHAN L. KLEIN
  - (B) REGISTRATION NUMBER: 41,119
  - (C) REFERENCE/DOCKET NUMBER: PF122P1D1
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 301-309-8504
  - (B) TELEFAX: 301-309-8439

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 444 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..441
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCC GGG AAC TCG ATC CTG CTG GCT GCT GTC TCT ATT CTC TCG GCC

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Asn | Ser | Ile | Leu | Leu | Ala | Ala | Val | Ser | Ile | Leu | Ser | Ala |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| TGT | CAG | CAA | AGT | TAT | TTT | GCT | TTG | CAA | GTT | GGA | AAG | GCA | AGA | TTA | AAA | 96  |
| Cys | Gln | Gln | Ser | Tyr | Phe | Ala | Leu | Gln | Val | Gly | Lys | Ala | Arg | Leu | Lys |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| TAC | AAA | GTT | ACG | CCC | CCA | GCA | GTC | ACT | GGG | TCA | CCA | GAG | TTT | GAG | AGA | 144 |
| Tyr | Lys | Val | Thr | Pro | Pro | Ala | Val | Thr | Gly | Ser | Pro | Glu | Phe | Glu | Arg |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| GTA | TTT | CGG | GCA | CAA | CAA | AAC | TGT | GTG | GAG | TTT | TAT | CCT | ATA | TTC | ATA | 192 |
| Val | Phe | Arg | Ala | Gln | Gln | Asn | Cys | Val | Glu | Phe | Tyr | Pro | Ile | Phe | Ile |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| ATT | ACA | TTG | TGG | ATG | GCT | GGG | TGG | TAT | TTC | AAC | CAA | GTT | TTT | GCT | ACT | 240 |
| Ile | Thr | Leu | Trp | Met | Ala | Gly | Trp | Tyr | Phe | Asn | Gln | Val | Phe | Ala | Thr |     |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| TGT | CTG | GGT | CTG | GTG | TAC | ATA | TAT | GGC | CGT | CAC | CTA | TAC | TTC | TGG | GGA | 288 |
| Cys | Leu | Gly | Leu | Val | Tyr | Ile | Tyr | Gly | Arg | His | Leu | Tyr | Phe | Trp | Gly |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| TAT | TCA | GAA | GCT | GCT | AAA | AAA | CGG | ATC | ACC | GGT | TTC | CGA | CTG | AGT | CTG | 336 |
| Tyr | Ser | Glu | Ala | Ala | Lys | Lys | Arg | Ile | Thr | Gly | Phe | Arg | Leu | Ser | Leu |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |
| GGG | ATT | TTG | GCC | TTG | TTG | ACC | CTC | CTA | GGT | GCC | CTG | GGA | ATT | GCA | AAC | 384 |
| Gly | Ile | Leu | Ala | Leu | Leu | Thr | Leu | Leu | Gly | Ala | Leu | Gly | Ile | Ala | Asn |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |     |
| AGC | TTT | CTG | GAT | GAA | TAT | CTG | GAC | CTC | AAT | ATT | GCC | AAG | AAA | CTG | AGG | 432 |
| Ser | Phe | Leu | Asp | Glu | Tyr | Leu | Asp | Leu | Asn | Ile | Ala | Lys | Lys | Leu | Arg |     |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |     |
| CGG | CAA | TTC | TAA |     |     |     |     |     |     |     |     |     |     |     |     | 444 |
| Arg | Gln | Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Gly | Asn | Ser | Ile | Leu | Leu | Ala | Ala | Val | Ser | Ile | Leu | Ser | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Cys | Gln | Gln | Ser | Tyr | Phe | Ala | Leu | Gln | Val | Gly | Lys | Ala | Arg | Leu | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Tyr | Lys | Val | Thr | Pro | Pro | Ala | Val | Thr | Gly | Ser | Pro | Glu | Phe | Glu | Arg |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Phe | Arg | Ala | Gln | Gln | Asn | Cys | Val | Glu | Phe | Tyr | Pro | Ile | Phe | Ile |  |

50                      55                      60  
 Ile Thr Leu Trp Met Ala Gly Trp Tyr Phe Asn Gln Val Phe Ala Thr  
 65                      70                      75                      80  
 Cys Leu Gly Leu Val Tyr Ile Tyr Gly Arg His Leu Tyr Phe Trp Gly  
                     85                      90                      95  
 Tyr Ser Glu Ala Ala Lys Lys Arg Ile Thr Gly Phe Arg Leu Ser Leu  
                     100                      105                      110  
 Gly Ile Leu Ala Leu Leu Thr Leu Leu Gly Ala Leu Gly Ile Ala Asn  
                     115                      120                      125  
 Ser Phe Leu Asp Glu Tyr Leu Asp Leu Asn Ile Ala Lys Lys Leu Arg  
                     130                      135                      140  
 Arg Gln Phe  
 145

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCGGGATCC GCCGGGAACG CGATCCTGCT GGCTGCT

37

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGCAAGCTT AGAATTGCCG CCTCAGTTTC TTGGC

35

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGGATCCGC CACCATGGCC GGGAACTCGA TCCT

34

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACAGGTACC AGCTTCTGCA AGCATTAAAG

30

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 160 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asp Gln Glu Thr Val Gly Asn Val Val Leu Leu Ala Ile Val Thr  
1 5 10 15

Leu Ile Ser Val Val Gln Asn Gly Phe Phe Ala His Lys Val Glu His  
20 25 30

Glu Ser Arg Thr Gln Asn Gly Arg Ser Phe Gln Arg Thr Gly Thr Leu  
35 40 45

Ala Phe Glu Arg Val Tyr Thr Ala Asn Gln Asn Cys Val Asp Ala Tyr  
50 55 60

Pro Thr Phe Leu Ala Val Leu Trp Ser Ala Gly Leu Leu Cys Ser Gln  
65 70 75 80

Val Pro Ala Ala Phe Ala Gly Leu Met Tyr Leu Phe Val Arg Gln Lys  
85 90 95

Tyr Phe Val Gly Tyr Leu Gly Glu Arg Thr Gln Ser Thr Pro Gly Tyr  
100 105 110

Ile Phe Gly Lys Arg Ile Ile Leu Phe Leu Phe Leu Met Ser Val Ala  
115 120 125

Gly Ile Phe Asn Tyr Tyr Leu Ile Phe Phe Gly Ser Asp Phe Glu Asn  
130 135 140

Tyr Ile Lys Thr Ile Ser Thr Thr Ile Ser Pro Leu Leu Leu Ile Pro  
145 150 155 160